This listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

Claims 1-28 (canceled)

Claim 29 (currently amended): A kit for detecting inactivation of a *CASP8* gene expression, comprising ~~*CASP8* gene-specific~~ oligonucleotide primers for amplification of at least a part of the 5' untranslated region of *CASP8* genomic DNA, wherein said primers are at least 10 nucleotides long and are used in a methylation polymerase chain reaction (PCR) assay.

Claims 30-55 (canceled)

Claim 56 (currently amended): A method for detecting inactivation of a *CASP8* gene expression in a primary cancer cell, comprising detecting ~~a~~ methylation of *CASP8* genomic DNA.

Claim 57 (currently amended): The method according to claim 56, wherein the methylation of *CASP8* genomic DNA is detected by a methylation polymerase chain reaction (PCR) assay.

Claim 58 (currently amended): The kit of claim 29, wherein the kit comprises ~~*CASP8* gene-specific~~ oligonucleotide PCR primers for amplification of SEQ ID NO: 1 or SEQ ID NO: 2.

Claim 59 (previously presented): The kit of claim 58, wherein the kit comprises at least one oligonucleotide PCR primer selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, and SEQ ID NO: 34.

Claim 60 (previously presented): The method according to claim 56, wherein the methylation occurs in the 5' untranslated region of *CASP8* genomic DNA.

Claim 61 (previously presented): The method according to claim 60, wherein the methylation occurs in sequences selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 2.

Claim 62 (previously presented): The method according to claim 57, wherein the PCR assay utilizes at least one of the primer sequences selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, and SEQ ID NO: 34.

Claims 63-65 (canceled)

Claim 66 (new): A method for prognosis of a neuroblastoma comprising detecting inactivation of a *CASP8* gene expression in a neuroblastoma cell from a subject, wherein said inactivation of a *CASP8* gene expression in the neuroblastoma cell is indicative of the inefficiency of apoptosis induced by activated death receptors, chemotherapeutic drugs, or irradiation, and wherein said method comprises detecting a methylation of *CASP8* genomic DNA.

Claim 67 (new): The method according to claim 66, wherein the neuroblastoma is a tumor in which a *myc* gene is amplified.

Claim 68 (new): The method according to claim 66, wherein the methylation of *CASP8* genomic DNA is detected by methylation polymerase chain reaction (PCR) assay.

Claim 69 (new): A method for diagnosis of an aggressive neuroblastoma comprising detecting inactivation of a *CASP8* gene expression in a neuroblastoma cell from a subject, wherein said inactivation of a *CASP8* gene expression in the neuroblastoma cell is indicative of the presence of an aggressive neuroblastoma and wherein said method comprises detecting a methylation of *CASP8* genomic DNA.

Claim 70 (new): The method according to claim 69, wherein the neuroblastoma is a tumor in which a *myc* gene is amplified.

Claim 71 (new): The method according to claim 69, wherein the methylation of *CASP8* genomic DNA is detected by methylation polymerase chain reaction (PCR) assay.

For Examiner's convenience, presented below are pending claims as amended arranged in order from independent to dependent:

Claim 56 (currently amended): A method for detecting inactivation of a *CASP8* gene expression in a primary cancer cell, comprising detecting ~~a~~ methylation of *CASP8* genomic DNA.

Claim 60 (previously presented): The method according to claim 56, wherein the methylation occurs in the 5' untranslated region of *CASP8* genomic DNA.

Claim 61 (previously presented): The method according to claim 60, wherein the methylation occurs in sequences selected from the group consisting of SEQ ID NO: 1 and SEQ ID NO: 2.

Claim 57 (currently amended): The method according to claim 56, wherein the methylation of *CASP8* genomic DNA is detected by a methylation polymerase chain reaction (PCR) assay.

Claim 62 (previously presented): The method according to claim 57, wherein the PCR assay utilizes at least one of the primer sequences selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, and SEQ ID NO: 34.

Claim 29 (currently amended): A kit for detecting inactivation of a *CASP8* gene expression, comprising ~~*CASP8* gene-specific~~ oligonucleotide primers for amplification of at least

a part of the 5' untranslated region of *CASP8* genomic DNA, wherein said primers are at least 10 nucleotides long and are used in a methylation polymerase chain reaction (PCR) assay.

Claim 58 (currently amended): The kit of claim 29, wherein the kit comprises ~~*CASP8* gene-specific~~ oligonucleotide PCR primers for amplification of SEQ ID NO: 1 or SEQ ID NO: 2.

Claim 59 (previously presented): The kit of claim 58, wherein the kit comprises at least one oligonucleotide PCR primer selected from the group consisting of SEQ ID NO: 29, SEQ ID NO: 30, SEQ ID NO: 31, SEQ ID NO: 32, SEQ ID NO: 33, and SEQ ID NO: 34.

Claim 66 (new): A method for prognosis of a neuroblastoma comprising detecting inactivation of a *CASP8* gene expression in a neuroblastoma cell from a subject, wherein said inactivation of a *CASP8* gene expression in the neuroblastoma cell is indicative of the inefficiency of apoptosis induced by activated death receptors, chemotherapeutic drugs, or irradiation, and wherein said method comprises detecting a methylation of *CASP8* genomic DNA.

Claim 67 (new): The method according to claim 66, wherein the neuroblastoma is a tumor in which a *myc* gene is amplified.

Claim 68 (new): The method according to claim 66, wherein the methylation of *CASP8* genomic DNA is detected by methylation polymerase chain reaction (PCR) assay.

Claim 69 (new): A method for diagnosis of an aggressive neuroblastoma comprising detecting inactivation of a *CASP8* gene expression in a neuroblastoma cell from a subject,

wherein said inactivation of a *CASP8* gene expression in the neuroblastoma cell is indicative of the presence of an aggressive neuroblastoma and wherein said method comprises detecting a methylation of *CASP8* genomic DNA.

Claim 70 (new): The method according to claim 69, wherein the neuroblastoma is a tumor in which a *myc* gene is amplified.

Claim 71 (new): The method according to claim 69, wherein the methylation of *CASP8* genomic DNA is detected by methylation polymerase chain reaction (PCR) assay.